

Genetic Variability and Character Association for Grain Yield and it's Related Traits in South Indian Rice (*Oryza sativa* L.) Varieties

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ABSTRACT: With current trend in the population growth, the demand for food in most parts of the world is increasing year by year. However, variability in yield among the crop species may be exhausted sooner or later, limiting the potential for additional crop improvement. As a result, understanding the genetic diversity of crop species is crucial for any crop improvement programmes. Hence the present investigation was carried out at Indian Institute of Rice Research, Hyderabad during kharif 2022 with 96 rice lines to assess the genetic variability for yield and its attributing traits. Analysis of variance revealed highly significant differences for all the traits studied. The estimates of PCV were slightly higher than the corresponding GCV for days to 50% flowering, days to maturity, plant height, panicle length, number of grains/panicle, weight of grains/panicle, 1000 grain weight and SPAD indicating that direct selection can be practiced for these characters. High heritability with high genetic advance were recorded for days to 50% flowering, flag leaf length & width, number of grains/panicle, weight of grains/panicle, 1000 grain weight and SPAD before booting indicating predominance of additive gene action. Correlation studies revealed that, the grain yield/plot had a significant and positive association with number of productive tillers/meter (0.27), weight of grains/panicle (0.32), biomass/plot (0.93) and harvest index (0.40). Tocher's clustering approach was used to group all genotypes into 10 clusters in which, cluster II was found to be the largest with 47 genotypes.

Keywords: Rice, Lattice design, Genetic variability, Correlation, Genetic diversity.

INTRODUCTION

Rice, commonly referred to as the “global grain” belongs to the family *Poaceae*, which is one of the few crop species endowed with the most genetic diversity. India is the second largest producer of rice next to China with an area of 46.38 m ha and production of 130.39 million tonnes with a productivity of 2809 kg/ha (Directorate of Economics and Statistics, 2022).

The genetic improvement of rice for yield and yield contributing traits is an important criteria to meet the food demand of the growing population (Rao *et al.*, 2021). As a result, the creation of genetic variability for improving yield and yield-attributing traits is a pre requisite in any crop improvement programme.

A systematic evaluation and characterization of germplasm lines along with the released and pre-released cultivars, not only aids in the discovery of superior and genetically divergent genotypes, but also provides knowledge regarding the value of genetic resources. The genetic improvement of quantitative characteristics present in the crop species is determined by the heritability pattern as well as the kind and quantity of diversity contained in the current

germplasm (Iraddi *et al.*, 2013). The magnitude of variation due to heritable component is very important, because it will guide in the selection of parents for crop improvement (Dutta *et al.*, 2013). Heritability estimates combined with genetic advances are usually more useful in predicting the gain under selection than heritability estimates alone.

The success of a breeding program depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable (Tiwari *et al.*, 2011). Genetic metrics like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) can be used to detect the degree of variability in germplasm.

Grain yield is a complex character, the knowledge of correlation between yield and yield component traits are of great importance in the selection of elite genotypes for breeding programmes (Dhavaleshvar *et al.*, 2019). Correlation coefficient analysis reveals the component traits on which parental selection can be done for genetic yield enhancement (Immanuel *et al.*, 2011). Correlation studies would give reliable data on the nature, size, and direction of selection, especially

when the breeder desires to combine high yield potentials with acceptable agronomic features and grain quality attributes.

Genetic divergence is an efficient tool for the effective choice of parents in hybridization programmes (Banumathy *et al.*, 2010). The D^2 approach (Mahalanobis, 1936), which is based on multivariate analysis, was discovered to be a powerful tool for assessing the degree of divergence in germplasm and developed genotypes. The Materials from genetically diverse and widely placed clusters is more divergent than the germplasm from the same cluster. As a result, categorising genotypes into distinct clusters will enable the breeders to choose the most genetically varied parents.

Therefore, for a successful breeding programme, thorough knowledge regarding the nature and magnitude of genetic variability along with character association in the crop species is a prerequisite.

MATERIAL AND METHODS

The present investigation was carried out at the Indian Institute of Rice Research Hyderabad during kharif 2022. The experimental material comprised of 96 south Indian rice genotypes collected from IIRR Hyderabad, ARS Marteru, ARS Jagtial, ARS Mandya etc. All recommended package of practices were adopted to raise a healthy nursery and 30 days old seedlings were transplanted to the main field in lattice design with two replication. Individual genotypes were assigned a plot size of $2m^2$ with four rows and a spacing of 20×15 cm. All recommended practices were implemented throughout the crop growing period to ensure a healthy crop. Observations were recorded on five randomly selected plants for yield and yield attributing characters namely: days to 50% flowering, days to maturity, plant height (cm), number of productive tillers/meter, flag leaf length(cm), flag leaf width(cm), panicle length (cm), number of grains/ panicle, weight of grains/panicle(g), 1000 grain weight, canopy temperature & SPAD before and after booting at 15 days interval, biomass/plot (g), grain yield/plot and harvest index.

The collected data were subjected to Analysis of variance by using SAS statistical software. The genotypic and phenotypic coefficients of variability were calculated using the Burton and Devane (1953) formula. Heritability was evaluated broadly according to Allard (1960) and characterised according to Johnson *et al.* (1955). The genetic advance was calculated based on the method given by Lush (1940). According to Johnson *et al.* (1955), the range of genetic advance was expressed as a percentage of the mean. The formulas proposed by Falconer (1981) were utilised to calculate correlation, and the Mahalanobis D^2 statistics were used to determine the genetic divergence. The genotypes were clustered by using Tochers method.

RESULTS AND DISCUSSION

ANOVA and Genetic parameters. The analysis of variance showed a substantial difference among the 96

genotypes for all the parameters studied, which indicates an appreciable amount of genetic variability among the genotypes. It also justifies the need for carrying out further genetic analysis and the scope for selecting suitable initial breeding material for crop improvement.

The parameters PCV and GCV, which denote the phenotypic and genotypic components, indicate the amount of variability present in the population. For all characters, the magnitude of PCV was found to be greater than the GCV, and there was only a slight disparity between PCV and GCV for majority of the traits (excluding harvest index), indicating a reduced effect of environmental variables on trait expression. Therefore, direct selection of these characters would be beneficial. Higher estimate of PCV and GCV (Table 1) were recorded for number of grains/ panicle (36.5, 34.0), 1000 grain weight (23.9, 23.6), and weight of grains/panicle (23.9, 20.3). These findings imply that there is enough variation among genotypes for these attributes to be directly selected or used in upcoming breeding operations. Similar results were obtained by Edukondalu *et al.* (2017); Bhargava *et al.* (2021) for number of grains/panicle, Rahman *et al.* (2014); Roy *et al.* (2015) for 1000 grain weight and Soni *et al.* (2013) for weight of grains/panicle. Moderate value of PCV and GCV were recorded for flag leaf length (19.1, 15.3), flag leaf width (17, 13.3), plant height (12.0, 10.4), days to 50% flowering (11.8, 11.7), SPAD before booting (12.8, 12.1), biomass/plot (14.7, 10.3) and grain yield/plot (15.9, 11.4). These results were similar to the findings of Sandeep *et al.* (2018) for plant height, Chakraborty and Chakraborty (2010) for flag leaf length & width, Adilakshmi and Rani (2012); Pandey *et al.* (2009) for biomass/plot. The measure of PCV and GCV were low for days to maturity (8.4, 8.2), canopy temperature before booting (4.26, 2.29), canopy temperature after booting (4.33, 3.38), SPAD after booting (9,7.9) and harvest index (7.11, 2.93), indicating minimal genotype-to-genotype variability for these parameters. Dhurai *et al.* (2014) obtained similar results for days to maturity and Yadav *et al.* (2017) for harvest index.

Variability among genotypes for several traits can be better utilised when they are heritable in nature. The results revealed that, majority of the traits exhibited high broad sense heritability (Table 1). It indicates that these characteristics are least affected by environmental factors, implying genetic modification through selection may be advantageous. The improvement of mean genotypic value of the chosen lines over mean genotypic value of the parental population is referred as genetic advancement, which is commonly stated as percentage of the mean. Selection solely based on broad sense heritability is deceptive since it is insufficiently informative about the existence of gene action (additive/non-additive) and the involvement of other variables in trait expression. Thus, heritability and genetic advancement work together to predict the genetic gain under selection (Johnson *et al.*, 1955).

Table 1: Mean, Range, GCV, PCV, Heritability (broad sense), Genetic Advance and Genetic Advance as per cent of mean for various traits.

Sr. No.	Characters	Mean	Range		Coefficient of variation (%)		Heritability (in broad sense) (%)	GA	GA as % of mean
			Min	Max	PCV	GCV			
1.	DFE	106	82	133	11.8	11.7	97.4	25.1	23.8
2.	DM	135	111	158	8.4	8.2	96.0	22.4	16.6
3.	Plant height	103	77	134	12.0	10.4	75.4	19.2	18.7
4.	PT	90	68	106	12.2	7.9	41.8	9.4	10.5
5.	FLL	32.0	21.6	52.6	19.1	15.3	63.9	8.0	25.2
6.	FLW	1.41	0.96	2.02	17.0	13.3	61.8	0.30	21.6
7.	PL	24.6	18.8	31.6	11.0	8.9	65.8	3.67	14.9
8.	G/P	222	108	485	36.5	34.0	87.1	145	65.4
9.	W/P	3.72	2.30	5.97	23.9	20.3	72.0	1.32	35.5
10.	TW	21.3	12.2	32.6	23.9	23.6	97.0	10.2	47.8
11.	CT-1	29.9	28.0	31.3	4.26	2.92	46.9	1.23	4.12
12.	CT-2	28.3	26.0	31.5	4.33	3.38	61.0	1.54	5.44
13.	SPAD-1	472	369	634	12.8	12.1	90.1	112	23.7
14.	SPAD-2	624	518	760	9.0	7.9	76.4	88.6	14.2
15.	Biomass	1520	1028	1920	14.7	10.3	48.9	225	14.8
16.	Y/P	424	260	570	15.9	11.4	51.2	71.2	16.8
17.	HI	0.28	0.24	0.33	7.11	2.93	16.93	0.01	2.48

Note: DFF = Days To 50% Flowering, DM = Days to Maturity, PT = Number of productive tillers/meter, FLL = Flag leaf length, FLW= Flag leaf width, PL= Panicle length, G/P = Number of grains/ panicle, W/P = Weight of grains/Panicle, TW = 1000 grain weight, CT-1 = Canopy Temperature before booting, CT-2 = Canopy Temperature after booting, SPAD-1: SPAD before booting, SPAD-2: SPAD after booting, Y/P = Grain yield/plot, HI = Harvest index

High heritability coupled with high genetic advance was recorded for days to 50% flowering, flag leaf length & width, number of grains/panicle, weight of grains/panicle, 1000 grain weight and SPAD before booting indicates predominance of additive gene action and the effectiveness of selection in these traits. The results are consistent with Padmaja *et al.* (2008) and Bhargavi *et al.* (2021). The days to maturity, plant height, panicle length and SPAD after booting exhibited high heritability along with moderate genetic advance as percent of the mean, suggesting a combined or conditional function of additive and non-additive gene activity in controlling these traits. In these case, high heritability may come from the positive effect of environmental variables. As a result, selection for these characteristics may be counter productive. The results are in conformity with Patel *et al.* (2014) and Islam *et al.* (2015) for Days to maturity, Sudeepthi *et al.* (2020) for plant height. The harvest index demonstrated low heritability with minimal genetic advance, indicating greater influence of environmental factors on this character.

Correlation and D² statistics. Correlation between yield and yield contributing traits were carried out for ninety six South Indian rice genotypes and the results were presented in Table 2. Correlation studies revealed that, grain yield/plot had a significant and positive association with traits such as number of productive tillers/meter (0.27), weight of grains/panicle (0.32), biomass/plot (0.93) and harvest index (0.40). Therefore, these traits were crucial for boosting production by increasing the yield. These results are in conformity with the results of Rashid *et al.* (2017) for number of productive tillers/meter, Nandeshwar *et al.* (2010); Bhadru *et al.* (2012); Soni *et al.* (2013) for weight of grains/panicle, Panwar (2005); Soni *et al.* (2013); Patel *et al.* (2014) for harvest index.

Similarly, it had negative significant association with canopy temperature before booting (-0.30) and after booting (-0.29) which is in accordance with Min *et al.* (2023). Grain yield/plot had positive non-significant association with plant height (0.17), flag leaf length (0.03), flag leaf width (0.12), panicle length (0.15), number of grains/ panicle (0.02), 1000 grain weight (0.14), and SPAD.

These results are in conformity with Madhavalatha *et al.* (2005); Hasan *et al.* (2013) for plant height, Moosavi *et al.* (2015) for panicle length, Rahman *et al.* (2014); Rashid *et al.* (2017) for number of grains/ panicle. Days to 50% flowering (-0.11) and days to maturity (-0.11) had negative non-significant association with grain yield/plot which was in accordance with Seyoum *et al.* (2012) for days to 50% flowering and Panwar (2005) for days to maturity.

Tocher's approach was used to arrange the genotypes into ten clusters based on D² values (Fig. 1). Out of the ten clusters obtained, cluster II was the largest with 47 genotypes followed by cluster I (39). Clusters III and V had 2 genotypes each, where as clusters IV, VI VII, VIII, IX and X were represented by single genotype indicating high degree of heterogeneity among the genotypes. Solitary clusters may emerge as a result of absolute isolation which prevents gene flow, or as a result of intense natural or human selection for various adaptive complexes. These genotypes may be quite distinct and valuable for breeding in future to increase the production and productivity.

The intra-cluster D² values (Table 3) varied from 0 to 149.4. Cluster II (149.4) had the greatest intra-cluster distance among the ten clusters followed by Cluster I (129.46), indicating that the genotypes in these clusters were genetically diverse. The genotypes carefully selected from these clusters can be used in future recombination breeding initiatives.

Table 2: Correlation co-efficient of yield and yield attributing traits.

	DFD	Mat	PH	PT	FLL	FLW	PL	G/P	W/P	TW	CR-1	CR-2	SPAD1	SPAD2	BM	HI	Y/P
DFD	1.00	0.97**	0.10	-0.15	0.16	0.38**	-0.03	0.56**	0.13	-0.46**	0.11	-0.30**	-0.14	-0.17	-0.08	-0.08	-0.11
DM		1.00	0.04	-0.15	0.10	0.36**	-0.06	0.53**	0.09	-0.46**	0.11	-0.29**	-0.14	-0.19	-0.08	-0.09	-0.11
PH			1.00	0.19	0.61**	0.41**	0.63**	0.24*	0.47**	0.09	-0.20	-0.44**	0.24*	0.27**	0.16	0.08	0.17
PT				1.00	0.16	-0.03	0.11	-0.10	0.02	0.24*	-0.04	-0.02	0.18	-0.04	0.24*	0.12	0.27**
FLL					1.00	0.38**	0.51**	0.19	0.35**	0.07	-0.09	-0.15	0.28**	0.09	-0.003	0.12	0.03
FLW						1.00	0.30**	0.64**	0.55**	-0.39**	-0.18	-0.14	0.40**	0.05	0.16	-0.07	0.12
PL							1.00	0.03	0.41**	0.27**	-0.16	-0.09	0.32**	0.16	0.19	-0.06	0.15
G/P								1.00	0.53**	-0.70**	0.04	-0.24*	0.11	-0.01	0.08	-0.12	0.02
W/P									1.00	0.06	0.01	-0.15	0.16	-0.07	0.35**	0.02	0.32**
TW										1.00	-0.002	0.16	-0.08	-0.05	0.10	0.12	0.14
CT-1											1.00	0.20	-0.37**	-0.28**	-0.37**	0.10	-0.30**
CT-2												1.00	0.22*	-0.16	-0.24*	-0.24*	-0.29**
SPAD1													1.00	0.14	0.20*	-0.18	0.12
SPAD2														1.00	-0.02	0.20	0.06
BM															1.00	0.03	0.93**
HI																1.00	0.40**
Y/P																	1.00

Note: DFD = Days To 50% Flowering, DM = Days to Maturity, PH = Plant Height, PT = Number of productive tillers/meter, FLL = Flag leaf length, FLW= Flag leaf width, PL= Panicle length, G/P = Number of grains/ panicle, W/P = Weight of grains/Panicle, TW = 1000 grain weight, CT-1 = Canopy Temperature before booting, CT-2 = Canopy Temperature after booting, SPAD 1 = SPAD before booting, SPAD 2 =SPAD after booting, BM = Biomass/plot, Y/P = Grain yield/plot, HI = Harvest index.

Table 3: Average inter and intra-cluster distances (D²) values of 96 rice genotypes.

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster9	Cluster10
Cluster1	129.5	273.6	228.1	338.4	338.8	444.9	326.8	461.3	257.8	349.1
Cluster2	273.6	149.4	547.0	267.2	306.8	240.9	258.4	254.0	283.2	733.9
Cluster3	228.1	547.0	39.8	365.5	574.0	601.5	448.9	593.2	449.9	313.1
Cluster4	338.4	267.2	365.5	0.0	574.2	84.5	164.2	105.1	275.0	815.9
Cluster5	338.8	306.8	574.0	574.2	66.2	630.6	671.6	595.8	623.9	720.4
Cluster6	444.9	240.9	601.5	84.5	630.6	0.0	186.4	100.4	236.6	1000.3
Cluster7	326.8	258.4	448.9	164.2	671.6	186.4	0.0	141.2	215.2	733.7
Cluster8	461.3	254.0	593.2	105.1	595.8	100.4	141.2	0.0	315.8	1088.9
Cluster9	257.8	283.2	449.9	275.0	623.9	236.6	215.2	315.8	0.0	681.0
Cluster10	349.1	733.9	313.1	815.9	720.4	1000.3	733.7	1088.9	681.0	0.0

The inter-cluster distance (Table 3) ranged from 84.46 to 1088.86. Clusters VIII and X had the longest and best inter- cluster distance (1088.86). Similarly, the relatively short inter-cluster distance was observed between clusters IV and VI (84.46). The larger the distance (D^2) between clusters, the higher the genetic divergence between cluster accessions (Ramayashree *et al.*, 2016). Crossing among the genotypes from different clusters improves the variability of gene pool. A considerable amount of variation was observed among the cluster means for all the traits (Table 4). The genotypes in cluster IX had maximum mean performance for grain yield/plot (455), biomass/plot (1680), flag leaf width (1.55), flag leaf length (52.6),

and plant height (133). Similarly, the genotypes in cluster X had minimum mean performance for grain yield/plot (300), SPAD after booting (374), canopy temperature on after booting (26.2), 1000 grain weight (12.2) and weight of grains/panicle (2.61).

Each trait's contribution to total diversity is calculated based on the number of times the character appears in the first rank (Table 5). Days to 50% flowering ranked first by contributing 42.86 % to total genetic divergence which is in accordance with Rathan *et al.* (2020). On the other hand, number of productive tillers/meter, flag leaf length, and harvest index appeared only once in first rank, indicating least contribution to total diversity.

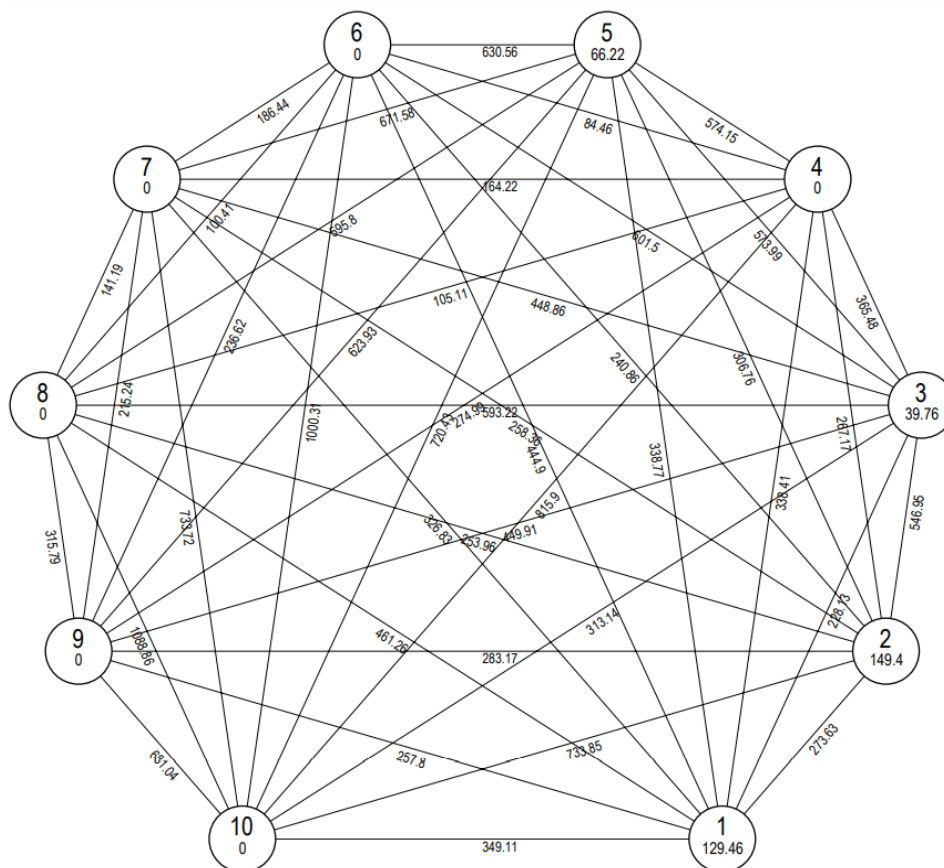


Fig. 1. Cluster diagram based on D^2 values by Tocher method.

Table 4: Cluster means for sixteen characters.

	DFE	Mat	PH	PT	FLL	FLW	PL	G/P	W/P	TW	CT-1	CT-2	SPAD 1	SPAD 2	BM	Y/P	HI
Cluster1	114	142	103	89	32.6	1.53	24.2	279	3.88	16.8	30.0	28.0	478	618	1537	429	0.28
Cluster2	98	128	103	91	31.4	1.31	25.0	172	3.66	25.1	30.0	28.5	470	626	1525	429	0.28
Cluster3	133	157	90	68	25.3	1.47	21.0	359	3.20	13.2	30.4	29.0	444	590	1372	362	0.26
Cluster4	120	152	94	98	24.9	1.53	24.1	158	3.49	27.4	30.8	29.1	416	576	1460	390	0.27
Cluster5	83	116.	94	86	31.0	1.51	23.4	208	3.00	16.4	28.9	28.9	549	671	1562	395	0.25
Cluster6	113	140	102	89	33.6	1.27	22.5	144	3.86	32.6	29.4	28.8	432	595	1410	370	0.26
Cluster7	118	146	116	94	35.8	1.39	28.3	184	4.18	26.0	29.4	26.7	384	686	1135	355	0.31
Cluster8	110	138	98	104	35.9	1.16	23.4	108	3.02	31.1	30.8	28.7	492	580	1568	420	0.27
Cluster9	119	149	133	86	52.6	1.55	28.0	202	3.79	23.6	28.0	26.8	544	654	1680	455	0.27
Cluster10	121	148	110	94	28.8	1.29	21.8	405	2.61	12.2	29.4	26.2	374	720	1145	300	0.26

Note: DFF = Days To 50% Flowering, DM = Days to Maturity, PH = Plant Height, PT = Number of productive tillers/meter, FLL = Flag leaf length, FLW= Flag leaf width, PL= Panicle length, G/P = Number of grains/ panicle, W/P = Weight of grains/Panicle, TW = 1000 grain weight, CT-1 = Canopy Temperature before booting, CT-2 = Canopy Temperature after booting, SPAD 1 = SPAD before booting, SPAD 2 =SPAD after booting, BM = Biomass/plot, Y/P = Grain yield/plot, HI = Harvest index.

Table 5: Relative contribution of different characters towards total genetic diversity.

Sr. No.	Characters	Times ranked 1st	Contribution %
1.	DFF	1357	42.86
2.	DM	18	0.56
3.	Plant height	16	0.50
4.	PT	1	0.03
5.	FLL	1	0.03
6.	FLW	7	0.21
7.	PL	7	0.21
8.	G/P	71	2.21
9.	W/P	105	3.27
10.	TW	810	25.24
11.	CT-1	91	2.83
12.	CT-2	64	1.99
13.	SPAD-1	410	12.78
14.	SPAD-2	220	6.85
15.	Biomass	11	0.34
16.	Y/P	2	0.06
17.	HI	1	0.03

Note: **DFF** = Days To 50% Flowering, **DM** = Days to Maturity, **PT** = Number of productive tillers/meter, **FLL** = Flag leaf length, **FLW**= Flag leaf width, **PL**= Panicle length, **G/P** = Number of grains/ panicle, **W/P** = Weight of grains/Panicle, **TW** = 1000 grain weight, **CT-1** = Canopy Temperature before booting, **CT-2** = Canopy Temperature after booting, **SPAD-1** = SPAD before booting, **SPAD-2** =SPAD after booting, **BM** = Biomass/plot, **Y/P** = Grain yield/plot, **HI** = Harvest index.

CONCLUSIONS

From the findings of present investigation, it can be concluded that a significant degree of genetic variation exists in ninety-six South Indian rice genotypes, since they displayed a broad range of variance for all of the traits evaluated.

Higher estimates of genetic parameters like PCV, GCV, broad sense heritability and genetic advance were observed for number of grains/panicle, weight of grains/panicle and 1000 grain weight indicating predominance of additive gene action. As a result, these traits are fixable and should be prioritised in future crop improvement programmes. The attributes such as, number of productive tillers/meter, weight of grains/panicle, biomass/plot, and harvest index might be utilised for yield enhancement, since they have a direct positive influence on grain yield/plot. D² analysis revealed that selected genotypes are highly diverse and are grouped into a total of 10 clusters. The accessions belonging to most distant clusters, namely (VIII and X), and (VI and X) might be used directly or as parents in the hybridization programme for yield improvement.

FUTURE SCOPE

The genotypes that are desirable for hybridization programme and the traits that are beneficial for yield improvement can be determined using current genetic variability investigations. This aids in designing the crossing programme and the development of selection parameters for increasing rice crop production.

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Conflict of Interest. None.

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